source AUTHORS TITLE JOURNAL AUTHORS TITLE JOURNAL REFERENCE TITTE JOURNA: TURES REFERENC COMMENT NUMAY, D. Marie., Metzer, M. Lee., Abramzon, S., Adams C., Alder, J., (Dases I to 1990s).

Allen, C., Allen, H., Albabrooks, S., Amin, A., Anguigho, D., Anyalbacchi, V., Aoyagi, R., Ayogij, M., Baca, E., Baden, B., Banamed, F., Baldardanaike, D., Barber, W., Barnspead, M., Benahmed, F., Blardardanaike, D., Barber, M., Barbarook, Brown, M., Baldir, J., Blankenburg, K., Blyth, C., Brown, M., Branalo, Y., Carter, Y., Caracas, T., Cardenae, V., Carter, A., Davag, C., Davy, Cartoll, C., Davy, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Flagg, M., Forbes, L., Foster, M., Foster, D., France, C.M., Gabisi, A., Oanga, S., Dunn, A. Durbin, K., Duval, B., Eaves, K., France, M., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Grill, R., Gracia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Grill, R., Gracia, A., Hogues, M., Havlak, P., Havlak, P., Havlak, R., Handun, M., Hernandez, J., Jackson, A., Hogues, M., Karpathy, S., Kally, S., Khan, C., Longake, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longake, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longake, S., Lopez, J., Lorensuhren, P., Marlin, K., Marxinez, E., Mandartne, M., Marxinez, E., Mandartne, M., Marxinez, E., Marier, S., Marxinez, S., Marker, M., Marxinez, D., Marker, M., Morris, S., Morris, S., Morris, S., Marier, S., 2535 1759 2595 1819 1879 JONN 190301 bp DNA linear HTG 19-NOV-2002 Rattus norvegicus clone CH230-442A4, WORKING DRAFT SEQUENCE, 2 2656 CCATCGTCACCGGGTACAGCGACCAGCAACCAGACATTTCCAACGGAAGCATTTGT 2715 ostomi; TGTTTCTTAAGCCCTGCAGCCCTTCGCGGAGTACGGACACTGAGCACAACCCCTGCGGGG TACCCAGTAACCCGGCCCAGGTGCCGATAGAGGAGTCCGGGGGCTTTGGCTCCCACCACC CCATCGTCACCGGTTACACCGACCAGCCTGATATCATCTCCAACGGAAGCATTTTGT Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute}6osto Mammalia; Eutheria; Rodentía; Sciurognathi; Muridae; Myfinae; Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Par
Pasternak,S., Paul,H., Perez,A., Perez,L., Ffannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., P.L.,L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., R DRAFT; HTGS_FULLTOP 1880 CCAACGAGACTAAACACCAGCGAGCAGAGCTC 1911 CCAACGAGGTAAGGCTGAAGGAAAGAAGCAC 2747 HTG: HTGS PHASE1; HTGS DRAFT; F Rattus norvegicus (Norway rat) Rattus norvegicus 119377.4 GI:25095811 (bases 1 to 190301) attus. 1640 1700 1820 2416 2596 1760 LOCUS CESSION KEYWORDS SOURCE AUTHORS REFERENCE AC119377 VERSION ORGAN g ઠે g ò ò q ò g ò

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Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F. Rives, C., Rodkey, T., Rolas, A., Rose, R., Rose, R., Ruiz, S. T. Sanders, W., Saverty, C., Scherer, S., Soct, G., Shatsman, S., Sherty, J., Stratebeyn, A., Sisson, I., Sitter, C.D., Smals, S., Shed, A., Sodergren, E., Song, X. Z., Sorelle, R., Sosa, J., Streine, M., Strong, R., Sutton, A., Svatek, A., Takor, P., Kaylor, T., Thomas, R., Sutton, A., Walek, A., Takor, P., Kaylor, C., Taylor, T., Thomas, N., Thomas, S. Tingey, A., Trejos, Z., Walas, R., Wallson, R., Warren, R., Waldron, L., Walker, F., Wallson, R., Willson, R., Warren, R., Wooden, H., Worley, K., Willson, R., Walch, S., Yen, J., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Duyh, D., von Wienstock, G. and Gibbs, R. A. Smith, Holl, Holling, Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-NOV-2002) Human Gefore Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor clustar and Human Genetics, Baylor College of Medicine, One Baylor clustar, Houston, TX 77036, USA.

On Nov 11, 2002 this sequency restion replaced gi:22856365.

The sequence in this assembly is a combination of BAC based reads and whole genome shorgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tm.ed/projects/rat/). Each contig described in the feature table below respressnts a scaffold in the Arlas assembly (a "contig-scaffold"). Within each contigs scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the erds of the clone and there may be sequence
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(see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence It currently
consists of 2 contigg. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigg are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Molecular and Human Genetics, Bayjor Coilege of Medicine, One Baylor Plaza, Houston, TX 77030, USP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contigs within a condig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Assemily program: Phash version 0.990329
Consensus quality: 174699 bases at least Q40
Consensus quality: 176582 bases at least Q30
Consensus quality: 177866 bases at least Q30
Estimated insert size: 181264; sum-of-contigs estimation
Obality coverage: 7x in Q20 bases; sum-of-contigs estimation
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188804 188903: gap of unknown length
188904 190301: contig of 1399 bp in length
Location/Qualifiers
1 190301
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Direct Submission
Submitted (26-APR-2002) Human Genome
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Rat (cenome Sequencing Consortium.)
Direct Submission
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Center project name: QV
Center plone name: CH2
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Web site: pttp://
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